CLAIMS

What is claimed is:

1. A method for reducing background in hybridization reactions of nucleic acids involving at least two homologous probes, wherein at least one of said probes is non-linear, comprising:

introducing a mismatch with an intended target sequence in at least one of the non-linear probes.

2. The method according to claim 1, wherein the homologous probes are designed to detect point mutations in at least one target sequence.

3. The method according to claim 1, wherein the at least one non-linear probe has a length from about 15 to about 50 nucleotides.

4. The method according to claim 1, wherein the at least one of the non-linear probes is provided with a detectable moiety.

5. The method according to claim 1, further comprising amplifying a nucleic acid sequence.

6. The method according to claim 1, wherein the mismatch comprises 1-3 nucleotides.

7. A method for reducing background in hybridization reactions of nucleic acids involving at least two homologous target sequences, comprising:

providing for an intended mismatch between at least one of the homologous target sequences and at least one non-linear probe for hybridization.

8. The method according to claim 2, wherein at least two of said non-linear probes and/or two of

said target sequences comprise an identical sequence except for a variation due to a point mutation or mismatch.

9. The method according to claim 2, wherein said mismatch is located between 2 and 20 nucleotides upstream or downstream of a point mutation.

10. The method according to claim 2, in which the homologous probes are designed to detect point mutations in at least one target sequence.

11. The method according to claim 2, wherein the mismatch in a nucleotide sequence comprises 1-3 nucleotides.

12. The method according to claim 2, wherein the at least one non-linear probe has a length from about 15 to about 50 nucleotides.

13. The method according to claim 2, wherein the at least one of the non-linear probes is provided with a detectable moiety.

14. The method according to claim 2, further comprising amplifying a nucleic acid sequence.

15. A method of detecting at least one allelic variant of a family of nucleic acids, said method comprising:

admixing a set of homologous probes for detection of at least one allelic variant of a family of nucleic acids and said family of nucleic acids, wherein at least one of said set of homologous probes is non-linear, said set of homologous probes comprising sequences complementary to and specific for one of the allelic variants of said family of nucleic acids, except for a specific mismatch located upstream or downstream from the site of variation;

hybridizing the set of homologous probes; and

detecting at least one allelic variant of the family of nucleic acids.

16. The method according to claim 15, wherein the family of nucleic acids is derived from a family of pathogens.

17. The method according to claim 16, wherein the family of nucleic acids represents a number of HIV-variants.

18. A set of mixed homologous probes for detection of at least one allelic variant of a nucleic acid family, wherein at least one of said set of mixed homologous probes is non-linear, said set of mixed homologous probes comprising at least one sequence complementary to and specific for one of the allelic variants of said nucleic acid family, except for a specific mismatch located upstream and/or downstream from the site of variation.

19. The set of mixed homologous probes of claim 18, wherein at least two of said probes comprise an identical sequence except for the site of variation.

20. The set of mixed homologous probes of claim 18, wherein said mismatch comprises 1-3 nucleotides.

21. The set of mixed homologous probes of claim 19, wherein said mismatch comprises 1-3 nucleotides.

22. The set of mixed homologous probes of claim 18, wherein said mismatch is located 2-20 nucleotides upstream or downstream of said site of variation.

23. The set of mixed homologous probes of claim 19, wherein said mismatch is located 2-20 nucleotides upstream or downstream of said site of variation.

24. The set of mixed homologous probes of claim 18, wherein the set of mixed homologous probes have lengths between about 15 and about 50 nucleotides.

25. The set of mixed homologous probes of claim 19, wherein the set of mixed homologous probes have lengths between about 15 and about 50 nucleotides.

26. The set of mixed homologous probes of claim 18, wherein said set of mixed homologous probes are in a single container.

27. The set of mixed homologous probes of claim 19, wherein said set of mixed homologous probes are in a single container.

28. A kit for the detection of at least one target sequence from a family of target sequences, comprising at least one non-linear probe complementary to a specific target sequence of said family of target sequences and having a mismatch in said complementarity for at least one of the target sequences from said family of target sequences and an detection system for said at least one target sequence.

29. A kit according to claim 28, comprising a set of mixed homologous probes for detection of at least one allelic variant of a family of target sequences, wherein at least one of said set of mixed homologous probes is non-linear, said set of mixed homologous probes comprising at least one sequence completely complementary to and specific for one of the allelic variants of said family of target sequences, except for a specific mismatch located upstream or downstream from a site of variation.

30. A kit according to claim 28, wherein said detection system comprises amplification of said at least one target sequence.

31. A kit according to claim 29, wherein said detection system comprises amplification of said at least one target sequence.

32. A kit according to claim 30, wherein said amplification of said at least one target sequence is selected from the group consisting of polymerase chain reaction (PCR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA) and transcription-mediated amplification (TMA).

33. A kit according to claim 28, wherein said detection system comprises isolation of said at least one target sequence.

34. A kit according to claim 29, wherein said detection system comprises isolation of said at least one target sequence.